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0321

OIPE

ENTERED

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/090,458

DATE: 03/19/2002
 TIME: 16:08:41

P.5

#2.

Input Set : A:\403.app
 Output Set: N:\CRF3\03192002\J090458.raw

4 <110> APPLICANT: Chen, Hongyun
 5 Kilinski, Ligia
 6 Le Bihan, Stephane
 9 <120> TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
 12 <130> FILE REFERENCE: 100103.403
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/090,458
 15 <141> CURRENT FILING DATE: 2002-03-01
 17 <160> NUMBER OF SEQ ID NOS: 5
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 5463
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: misc_feature
 28 <222> LOCATION: 25, 2888, 2889
 29 <223> OTHER INFORMATION: n. = A,T,C or G
 32 <400> SEQUENCE: 1
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 34 gcgtccaggc ctgacagctc tgcggctcgg gccctgaggt ttattcagaa aacatgtcca 120
 35 ctgcaattag ggaggttaga gtttgagac agaccagaac acttctactg aagaattact 180
 36 taattaaatg cagaaccaa aagagtagtg ttcaggaaat tctttttcca ctattttttt 240
 37 ttttttggtt aatattaatt agcatgatgc atccaaataa gaaatatgaa gaagtgccta 300
 38 atatagaact caatcctatg gacaagttaa ctctttctaa tctaattctt ggatatactc 360
 39 cagtgactaa tattacaagc agcatcatgc agaaagtgtc tactgatcat ctacctgatg 420
 40 tcataattac tgaagaatat acaaatgaaa aagaaatgtt aacatccagt ctctctaagc 480
 41 cgagcaactt tgtaggtgtg gttttcaaaag actccatgtc ctatgaactt cgtttttttc 540
 42 ctgatatgat tccagtatct tctatttata tggattcaag agctggctgt tcaaaatcat 600
 43 gtgaggctgc tcagtactgg tcctcaggtt tcacagtttt acaagcatcc atagatgctg 660
 44 ccattataca gttgaagacc aatgtttctc tttggaagga gctggagtca actaaagctg 720
 45 ttattatggg agaaactgct gttgtagaaa tagatacctt tccccgagga gtaattttta 780
 46 tatacctagt tatagcattt tcaccttttg gatacttttt ggcaattcat atcgtagcag 840
 47 aaaaagaaaa aaaaataaaa gaatttttaa agataatggg acttcatgat actgcctttt 900
 48 ggctttcctg ggttcttcta tatacaagtt taatttttct tatgtccctt cttatggcag 960
 49 tcattgcgac agcttctttg ttatttcctc aaagtagcag cattgtgata tttctgcttt 1020
 50 ttttctttta tggattatca tctgtatttt ttgctttaat gctgacacct ctttttaaaa 1080
 51 aatcaaaaca tgtgggaata gttgaatttt ttgttactgt ggcttttgga tttattggcc 1140
 52 ttatgataat cctcatagaa agttttccca aatcgttagt gtggttttcc agtccctttc 1200
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 56 gggaaatttg cttacggaga tcatctttat attttctgaa gccttcatat tgggtcaaaga 1440
 57 gcaaaagaaa ttatgaggag ttatcagagg gcaatgttaa tggaaatatt agtttttagt 1500

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58 aaattattga gccagtttct tcagaatttg taggaaaaga agccataaga attagtggta 1560
59 ttcagaagac atacagaaaag aagggtgaaa atgtggaggc tttgagaaat ttgtcatttg 1620
60 acatatatga gggtcagatt actgccttac ttggccacag tggaacagga aagagtacat 1680
61 tgatgaatat tctttgtgga ctctgcccac cttctgatgg gtttgcatct atatatggac 1740
62 acagagtctc agaaatagat gaaatgtttg aagcaagaaa aatgattggc atttgtccac 1800
63 agttagatat acactttgat gttttgacag tagaagaaaa tttatcaatt ttggcttcaa 1860
64 tcaaagggat accagccaac aatataatac aagaagtgca gaaggtttta ctagatttag 1920
65 acatgcagac tatcaaagat aaccaagcta aaaaattaag tgggtggtcaa aaaagaaagc 1980
66 tgtcattagg aattgctggt cttgggaacc caaagatact gctgctagat gaaccaacag 2040
67 ctggaatgga cccctgttct cgacatatgt tagggaatct tttaaaatac agaaaagcca 2100
68 atcgggtgac agtggttcagt actcatttca tggatgaagc tgacattctt gcagatagga 2160
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82 taatggtgac gatgattaat gacagtgact atgtatccgt ggctcccat agtgcggtt 3000
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103 gtgaagatga tgattcactg aagtgtatgg gttactgtcc tcagataaac cctttgtggc 4260
104 cagatactac attgcaggaa cattttgaaa tttatggagc tgtcaagga atgagtgcaa 4320
105 gtgacatgaa agaagtcata agtcgaataa cacatgcact tgatttaaaa gaacatcttc 4380
106 agaagactgt aaagaaacta cctgcaggaa tcaaacgaaa gttgtgtttt gctctaagta 4440

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107 tgctagggaa tcctcagatt accttgctag atgaaccatc tacaggtatg gatcccaaag 4500
108 ccaaacagca catgtggcga gcaattcgaa ctgcatttaa aaacagaaaag cgggctgcta 4560
109 ttctgaccac tcactatatg gaggaggcag aggctgtctg tgatcgagta gctatcatgg 4620
110 tgtctgggca gttaagatgt atcggaacag tacaacatct aaagagtaaa tttggaaaag 4680
111 gctacttttt ggaaattaaa ttgaaggact ggatagaaaa cctagaagta gaccgccttc 4740
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113 tggcttataa aattcctaag gaagatgttc agtccctttc acaatctttt ttaagctgg 4860
114 aagaagctaa acatgctttt gccattgaag aatatagctt ttctcaagca acattggaac 4920
115 aggtttttgt agaactcact aaagaacaag aggaggaaga taatagttgt ggaactttaa 4980
116 acagcacact ttggtgggaa cgaacacaag aagatagagt agtattttga atttgatttg 5040
117 ttcggtctgc ttactgggac ttctttcttt ttcaactaat ttttaacttg gtttaaaaag 5100
118 ttttttattg gaatggtaac tggagaacca agaacgcact tgaaattttt ctaagctcct 5160
119 taattgaaat gctgtggttg tgtgttttgc ttttctttta ataaaacgta tgtataatta 5220
120 agtgaagctg catgtttgta ttgaagtata ttgaactata tagtttgat gtcactttt 5280
121 tcaccattca gaaacagtgc ttctgaattt gtgattttaa ggaattgtaa tagaatagtt 5340
122 ttatttttaa gttatcttta agtttatgcc atcttcttaa ataagtacgt aatgttccaa 5400
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124 gtt 5463

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126 <210> SEQ ID NO: 2

127 <211> LENGTH: 1638

128 <212> TYPE: PRT

129 <213> ORGANISM: Homo sapiens

131 <220> FEATURE:

132 <221> NAME/KEY: VARIANT

133 <222> LOCATION: 926

134 <223> OTHER INFORMATION: Xaa = Any Amino Acid

137 <400> SEQUENCE: 2

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138 Met Ser Thr Ala Ile Arg Glu Val Gly Val Trp Arg Gln Thr Arg Thr
139 1 5 10 15
140 Leu Leu Leu Lys Asn Tyr Leu Ile Lys Cys Arg Thr Lys Lys Ser Ser
141 20 25 30
142 Val Gln Glu Ile Leu Phe Pro Leu Phe Phe Leu Phe Trp Leu Ile Leu
143 35 40 45
144 Ile Ser Met Met His Pro Asn Lys Lys Tyr Glu Glu Val Pro Asn Ile
145 50 55 60
146 Glu Leu Asn Pro Met Asp Lys Phe Thr Leu Ser Asn Leu Ile Leu Gly
147 65 70 75 80
148 Tyr Thr Pro Val Thr Asn Ile Thr Ser Ser Ile Met Gln Lys Val Ser
149 85 90 95
150 Thr Asp His Leu Pro Asp Val Ile Ile Thr Glu Glu Tyr Thr Asn Glu
151 100 105 110
152 Lys Glu Met Leu Thr Ser Ser Leu Ser Lys Pro Ser Asn Phe Val Gly
153 115 120 125
154 Val Val Phe Lys Asp Ser Met Ser Tyr Glu Leu Arg Phe Phe Pro Asp
155 130 135 140
156 Met Ile Pro Val Ser Ser Ile Tyr Met Asp Ser Arg Ala Gly Cys Ser
157 145 150 155 160
158 Lys Ser Cys Glu Ala Ala Gln Tyr Trp Ser Ser Gly Phe Thr Val Leu
159 165 170 175

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```

160 Gln Ala Ser Ile Asp Ala Ala Ile Ile Gln Leu Lys Thr Asn Val Ser
161      180      185      190
162 Leu Trp Lys Glu Leu Glu Ser Thr Lys Ala Val Ile Met Gly Glu Thr
163      195      200      205
164 Ala Val Val Glu Ile Asp Thr Phe Pro Arg Gly Val Ile Leu Ile Tyr
165      210      215      220
166 Leu Val Ile Ala Phe Ser Pro Phe Gly Tyr Phe Leu Ala Ile His Ile
167 225      230      235      240
168 Val Ala Glu Lys Glu Lys Lys Ile Lys Glu Phe Leu Lys Ile Met Gly
169      245      250      255
170 Leu His Asp Thr Ala Phe Trp Leu Ser Trp Val Leu Leu Tyr Thr Ser
171      260      265      270
172 Leu Ile Phe Leu Met Ser Leu Leu Met Ala Val Ile Ala Thr Ala Ser
173      275      280      285
174 Leu Leu Phe Pro Gln Ser Ser Ser Ile Val Ile Phe Leu Leu Phe Phe
175      290      295      300
176 Leu Tyr Gly Leu Ser Ser Val Phe Phe Ala Leu Met Leu Thr Pro Leu
177 305      310      315      320
178 Phe Lys Lys Ser Lys His Val Gly Ile Val Glu Phe Phe Val Thr Val
179      325      330      335
180 Ala Phe Gly Phe Ile Gly Leu Met Ile Ile Leu Ile Glu Ser Phe Pro
181      340      345      350
182 Lys Ser Leu Val Trp Leu Phe Ser Pro Phe Cys His Cys Thr Phe Val
183      355      360      365
184 Ile Gly Ile Ala Gln Val Met His Leu Glu Asp Phe Asn Glu Gly Ala
185      370      375      380
186 Ser Phe Ser Asn Leu Thr Ala Gly Pro Tyr Pro Leu Ile Ile Thr Ile
187 385      390      395      400
188 Ile Met Leu Thr Leu Asn Ser Ile Phe Tyr Val Leu Leu Ala Val Tyr
189      405      410      415
190 Leu Asp Gln Val Ile Pro Gly Glu Phe Gly Leu Arg Arg Ser Ser Leu
191      420      425      430
192 Tyr Phe Leu Lys Pro Ser Tyr Trp Ser Lys Ser Lys Arg Asn Tyr Glu
193      435      440      445
194 Glu Leu Ser Glu Gly Asn Val Asn Gly Asn Ile Ser Phe Ser Glu Ile
195      450      455      460
196 Ile Glu Pro Val Ser Ser Glu Phe Val Gly Lys Glu Ala Ile Arg Ile
197 465      470      475      480
198 Ser Gly Ile Gln Lys Thr Tyr Arg Lys Lys Gly Glu Asn Val Glu Ala
199      485      490      495
200 Leu Arg Asn Leu Ser Phe Asp Ile Tyr Glu Gly Gln Ile Thr Ala Leu
201      500      505      510
202 Leu Gly His Ser Gly Thr Gly Lys Ser Thr Leu Met Asn Ile Leu Cys
203      515      520      525
204 Gly Leu Cys Pro Pro Ser Asp Gly Phe Ala Ser Ile Tyr Gly His Arg
205      530      535      540
206 Val Ser Glu Ile Asp Glu Met Phe Glu Ala Arg Lys Met Ile Gly Ile
207 545      550      555      560
208 Cys Pro Gln Leu Asp Ile His Phe Asp Val Leu Thr Val Glu Glu Asn

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
Input Set : A:\403.app

Output Set: N:\CRF3\03192002\J090458.raw

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209          565          570          575
210 Leu Ser Ile Leu Ala Ser Ile Lys Gly Ile Pro Ala Asn Asn Ile Ile
211          580          585          590
212 Gln Glu Val Gln Lys Val Leu Leu Asp Leu Asp Met Gln Thr Ile Lys
213          595          600          605
214 Asp Asn Gln Ala Lys Lys Leu Ser Gly Gly Gln Lys Arg Lys Leu Ser
215          610          615          620
216 Leu Gly Ile Ala Val Leu Gly Asn Pro Lys Ile Leu Leu Leu Asp Glu
217 625          630          635          640
218 Pro Thr Ala Gly Met Asp Pro Cys Ser Arg His Ile Val Trp Asn Leu
219          645          650          655
220 Leu Lys Tyr Arg Lys Ala Asn Arg Val Thr Val Phe Ser Thr His Phe
221          660          665          670
222 Met Asp Glu Ala Asp Ile Leu Ala Asp Arg Lys Ala Val Ile Ser Gln
223          675          680          685
224 Gly Met Leu Lys Cys Val Gly Ser Ser Met Phe Leu Lys Ser Lys Trp
225          690          695          700
226 Gly Ile Gly Tyr Arg Leu Ser Met Tyr Ile Asp Lys Tyr Cys Ala Thr
227 705          710          715          720
228 Glu Ser Leu Ser Ser Leu Val Lys Gln His Ile Pro Gly Ala Thr Leu
229          725          730          735
230 Leu Gln Gln Asn Asp Gln Gln Leu Val Tyr Ser Leu Pro Phe Lys Asp
231          740          745          750
232 Met Asp Lys Phe Ser Gly Leu Phe Ser Ala Leu Asp Ser His Ser Asn
233          755          760          765
234 Leu Gly Val Ile Ser Tyr Gly Val Ser Met Thr Thr Leu Glu Asp Val
235          770          775          780
236 Phe Leu Lys Leu Glu Val Glu Ala Glu Ile Asp Gln Ala Asp Tyr Ser
237 785          790          795          800
238 Val Phe Thr Gln Gln Pro Leu Glu Glu Glu Met Asp Ser Lys Ser Phe
239          805          810          815
240 Asp Glu Met Glu Gln Ser Leu Leu Ile Leu Ser Glu Thr Lys Ala Ala
241          820          825          830
242 Leu Val Ser Thr Met Ser Leu Trp Lys Gln Gln Met Tyr Thr Ile Ala
243          835          840          845
244 Lys Phe His Phe Phe Thr Leu Lys Arg Glu Ser Lys Ser Val Arg Ser
245          850          855          860
246 Val Leu Leu Leu Leu Ile Phe Phe Thr Val Gln Ile Phe Met Phe
247 865          870          875          880
248 Leu Val His His Ser Phe Lys Asn Ala Val Val Pro Ile Lys Leu Val
249          885          890          895
250 Pro Asp Leu Tyr Phe Leu Lys Pro Gly Asp Lys Pro His Lys Tyr Lys
251          900          905          910
W--> 252 Thr Ser Leu Leu Gln Asn Ser Ala Gly Glu Ser Val Xaa Glu Asp
253          915          920          925
254 Ser Asp Ile Ser Asp Leu Ile Ser Phe Phe Thr Ser Gln Asn Ile Met
255          930          935          940
256 Val Thr Met Ile Asn Asp Ser Asp Tyr Val Ser Val Ala Pro His Ser
257 945          950          955          960

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 Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/090,458

DATE: 03/19/2002

TIME: 16:08:42

Input Set : A:\403.app

Output Set: N:\CRF3\03192002\J090458.raw

L:14 M:270 C: Current Application Number differs, Wrong Format
L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4